```
(5')    1  SDLEQERRAKEKLQEQQ
       18  SDLEQDRLAKEKLQEQQ
       35  SDLEQERLAKEKLQEQQ
       52  SDLEQERRAKEKLQEQQ
       69  SDLEQERRAKEKLQEQQ
       86  SDLEQDRLAKEKLQEQQ
      103  SDLEQERRAKEKLQEQQ
      120  SDLEQERRAKEKLQEQQ
      137  SDLEQERLAKEKLQEQQ
      154  SDLEQERRAKEKLQEQQ
      171  SDLEQERRAKEKLQEQQ
      188  SDLEQERRAKEKLQEQQ
      205  RDLEQ


      210  RKADTKKNLERKKEHGDILAEDLYGRLEIP
      240  AIELPSENERGYYIPHQSSLPQDNRGNSRD
      270  SKEISIIEKTNRESITTNVEGRRDIHKGHL
      300  EEKKDGSIKPEQKEDKS    316 (3')
```

FIGURE 1

```
(5')   1  AAAGCCGATCTCTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
      52  AAAGCCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
     103  AAAGCCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
     154  AAAGCCGATCTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     205  AAAGCCGATTTAGAACAAGAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     256  AAAGCCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
     307  AAAGCCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     358  AAAGCCGATTTAGAACAAGAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     409  AAAGCCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
     460  AAAGCCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     511  AAAGCCGATTTAGAACAAGAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     562  AAAGCCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC
     613  AAAGAGATTTAGAACAA
     630  AGGAAGGCTGATACGAAAAAAATTTAGAAGAAAAGGAACATGGAGAT
     681  ATATTAGCAGAGGATTTATGTCGTTTAGAAATACCAGCTATAGAACTT
     732  CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
     783  CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
     834  AAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
     885  CATAAAGGACATCTTGAAGAAAGAAGATGGTTCAATAAAACCAGAACAA
     936  AAAGAAGATAAATCT   950  (3')
```

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVJSVQQEQQ

HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI

ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE

ESVAPSVEESVAEMLKER

FIGURE 3

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT
GTT AAT GGA GAA GTA AAA GAA AAT ATT TTG GAG GAA AGT CAA GTT AAT
GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA
CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG
AAG AAA GTG TAG AAG AAA ATG TAG AAG AAA ATG TAG AAG AAA ATG
ACG ACG GAA GTG TAG CCT CAA GTG TTG AAG GTA TAG CTT CAA GTG
TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG AAA ATG TAG CTC CAA CTG
TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG AAA TTG TAG CTC CAA GTG
TTG TAG AAA AGT GTG CTC CAA GTG TTG AAG AAA GTG TAG CTC CAA GTG
TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

NSRDSKEISIIEKTNRESITTNVEGRRDIHK   LSA-TER

DELFNELLNSVDVNGEVKENILEESQ   729S-NRI
LEESQVNDDIFSNSLVKSVQQEQQHNV   729S-NRII
VEKCAPSVEESVAPSVEESVAEMLKER   729S-Rep

FIGURE 5

NUCLEOTIDE SEQUENCE OF THE LSA GENE
5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

```
33  ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
84  ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA
186 GGAAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAACT
237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT
288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAGTCTTTTAAGAAATCT
339 TGGTGTTTCAGAGAATATATTCCTTAAAGAAAATAAATTAAATAAGGAAGGG
390 AAATTAATTGAACACATAATAAATGATGATGACGATAAAAAAAAATATATTA
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCA
```

(CODING 5' END, repetitive)

```
492 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGT
543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
594 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT
900 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988
```

FIGURE 6

LSA.5'/ATG - -> 1-phase Translation

DNA sequence 956 b.p. ATGAAACATATT ... AAGCGATTTAGA linear

```
1   /   1
ATG AAA CAT ATT TTG TAC ATA TCA TTT TAC TTT ATC CTT GTT AAT TTA TTG ATA TTT CAT
met lys his ile leu tyr ile ser phe tyr phe ile leu val asn leu leu ile phe his
61  /  21
ATA AAT GGA AAG ATA ATA AAG AAT TCT GAA AAA GAT GAA ATC ATA AAA TCT AAC TTG AGA
ile asn gly lys ile ile lys asn ser glu lys asp glu ile ile lys ser asn leu arg
121 /  41
AGT GGT TCT TCA AAT TCT AGG AAT CGA ATA AAT GAG GAA AAT CAC GAG AAG AAA CAC GTT
ser gly ser ser asn ser arg asn arg ile asn glu glu asn his glu lys lys his val
181 /  61
TTA TCT CAT AAT TCA TAT GAG AAA ACT AAA AAT GAA AAT AAT AAA TTT TTC GAT AAG
leu ser his asn ser tyr glu lys thr lys asn asn glu asn asn lys phe phe asp lys
241 /  81
GAT AAA GAG TTA ACG ATG TCT AAT GTA AAA AAT GTG TCA CAA ACA AAT TTC AAA AGT CTT
asp lys glu leu thr met ser asn val lys asn val ser gln thr asn phe lys ser leu
301 / 101
TTA AGA AAT CTT GGT GTT TCA GAG AAT ATA TTC CTT AAA GAA AAT AAA TTA AAT AAG GAA
leu arg asn leu gly val ser glu asn ile phe leu lys glu asn lys leu asn lys glu
```

FIGURE 7A

```
361 /  121                          391 /  131
GGG AAA TTA ATT GAA CAC ATA GAT GAC GAT   AAA AAA TAT ATT AAA GGG
gly lys leu ile glu his ile asp asp asp   lys lys tyr ile lys gly

421 /  141                          451 /  151
CAA GAC AAC AGA CAA GAA GAT   CTT GAA AAA GCT AAA GAA TTA CAG GGG
gln asp asn arg gln glu asp   leu glu lys ala lys glu leu gln gly

481 /  161                          511 /  171
CAA CAA AGC GAT TCA GAA CAA GAG   CGT GCT AAA GAA CAA CAA AGC
gln gln ser asp ser glu gln glu   arg ala lys glu gln gln ser

541 /  181                          571 /  191
GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA   TTA GAA CAA GAG AGA
asp leu glu gln glu arg leu ala lys glu   leu glu gln glu arg

601 /  201                          631 /  211
CAA GAG AGA CGT GCT AAA GAA TTG CAA   GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA
gln glu arg arg ala lys glu leu gln   glu gln gln ser asp leu glu gln glu arg

661 /  221                          691 /  231
CTT GCT AAA GAA TTG CAA CAA GAA CAA CAA AGC   GAT TTA GAA CAA GAG CGT GCT AAA
leu ala lys glu leu gln gln glu gln gln ser   asp leu glu gln glu arg ala lys

721 /  241                          751 /  251
GAA AAG TTG CAA GAA CAA CAA AGC   GAT TTA GAA CAA GAA AAG TTG
glu lys leu gln glu gln gln ser   asp leu glu gln glu lys leu
```

FIGURE 7B

```
781 /  261
CAA GAA CAA CAA AGC GAT TTA GAA CAA AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG
gln glu gln gln ser asp leu glu gln arg leu ala lys glu lys leu gln glu gln
                              811 /  271

841 /  281
CAA AGC GAT TTA GAA CAA GAT TTA GCT AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT
gln ser asp leu glu gln asp leu ala arg leu ala lys glu lys leu gln glu gln ser asp
                              871 /  291

901 /  301
TTA GAA CAA GAG AGA CGT GCT AAA GAA AGG TTA CAA GAA CAA CAA AGC GAT TTA
leu glu gln glu arg arg ala lys glu arg leu gln glu gln gln ser asp leu
                              931 /  311
```

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE
3' END

(CODING 3' END, REPETITIVE)

```
1   CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
37  GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
88  GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
190 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
241 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
343 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
445 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
598 GCTAAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA
```

(CODING 3' END, UNIQUE)

```
640  AGGAAGGCTGATACGAAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
691  ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
742  CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
793  CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
844  AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
895  CATAAAGGACATCTTGAAGAAAGAAAGATGGTTCAATAAAACCAGAACAA
946  AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT
997  ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
1252 AAAAAATAAAAAAAAGGAAAGAAATATGAAAAAACAAAGGATAATAATTTTA
1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA
1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
1456 ATATAACTAAATATTTTATGAAACTATAA (stop)
```

(NON-CODING 3' END)

```
1485 AAGGTTATATATTT 1498
```

FIGURE 8

LSA.3'.ALL -> 1-phase Translation

DNA sequence 1496 b.p.   CAAGAACAACAA ... GGTTATATATT   linear

```
1 / 1                          31 / 11
CAA GAA CAA CAA AGC GAT CTA GAA CAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA
gln glu gln gln ser asp leu glu gln gln glu arg arg ala lys glu lys leu gln glu gln
61 / 21                        91 / 31
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAA AAG TTA CAA GAG CAG CAA AGC GAT
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu lys leu gln glu gln gln ser asp
121 / 41                       151 / 51
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA
leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu glu gln
181 / 61                       211 / 71
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG CAA AGA CGT
glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu arg arg
241 / 81                       271 / 91
GCT AAA GAA AAG TTG CAA GAA CAA CAA GAT AGA CTT GCT AAA GAA
ala lys glu lys leu gln glu gln gln asp arg leu ala lys glu
301 / 101                      331 / 111
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG CAA AGA CGT GCT AAA GAA AAG TTG CAA
lys leu gln glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln
```

FIGURE 9A

```
361                                                      / 121
GAA CAA AGC GAT TTA GAA CAA AGC GAT TTA GAA CAA AGA CGT GCT AAA GAA AAG TTG CAA
glu gln ser asp leu glu gln ser asp leu glu gln arg arg ala lys glu lys leu gln
                                       391               / 131

421                                                      / 141
GAA CAA CAA GAG AGG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA
glu gln gln glu arg arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln
                                       451               / 151

481                                                      / 161
AGC GAT TTA GAA CAA CAA GAG AGG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA GAG
ser asp leu glu gln gln glu arg arg arg ala lys glu lys leu gln glu gln gln glu
                                       511               / 171

541                                                      / 181
AGG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA CAA GAG CAA GAG
arg arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln gln glu gln glu
                                       571               / 191

601                                                      / 201
AGA CGT GCT AAA GAA AAG TTG CAA GAG GAG CAA GAG GAT TTA GAA CAA CAA GAG AGG AAG
arg arg ala lys glu lys leu gln glu glu gln glu asp leu glu gln gln glu arg lys
                                       631               / 211

661                                                      / 221
AAA GAA AAG TTG CAA GAG GAG CAA GAG GAT ATA TTA GCA GAG GAT TTA GAA GAT ATA TTA
lys glu lys leu gln glu glu gln glu asp ile leu ala glu asp leu glu asp ile leu
                                       691               / 231

721                                                      / 241
AAT TTA GAA AGA AAG AAG GAA GAT ATA TTA GAA ATA GAA ATA CCA GCT ATA GAA CAT CAA
asn leu glu arg lys lys glu asp ile leu glu ile glu ile pro ala ile glu his gln
                                       751               / 251

781                                                      / 261
TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA
ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile
                                       811               / 271
```

FIGURE 9B

```
841 /     281
GAA AAA ACA AAT AGA GAA TCT ATT ACA ACA  AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA
glu lys thr asn arg glu ser ile thr thr  asn val glu gly arg arg asp ile his lys
                              871 /  291
901 /     301
GGA CAT CTT GAA AAG GAA GAA AAG GAT GGT  TCA ATA AAA CCA GAA CAA AAA GAT GAA TCT
gly his leu glu lys glu glu lys asp gly  ser ile lys pro glu gln lys glu asp lys ser
                              931 /  311
961 /     321
GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA  GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA
ala asp ile gln asn his thr leu glu thr  val asn ile ser asp val asn asp phe gln
                              991 /  331
1021 /    341
ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT  GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA
ile ser lys tyr glu asp glu ile ser ala  glu tyr asp asp ser leu ile asp glu glu
                              1051 / 351
1081 /    361
GAA GAT GAT GAA GAC TTA GAC GAA TTT AAG  CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT
glu asp asp glu asp leu asp glu phe lys  pro ile val gln tyr asp asn phe gln asp
                              1111 / 371
1141 /    381
GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA  GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA
glu glu asn ile gly ile tyr lys glu leu  glu asp leu ile glu lys asn glu asn leu
                              1171 / 391
1201 /    401
GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA  TCA GAA GAA TTA TCT GAA GAA AAA ATA AAA
asp asp leu asp glu gly ile glu lys ser  ser glu glu leu ser glu glu lys ile lys
                              1231 / 411
```

FIGURE 9C

```
1261 /   421                1291 /   431
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
lys gly lys lys tyr glu lys thr lys asp asn asn phe lys pro asn asp lys ser leu
1321 /   441                1351 /   451
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys
1381 /   461                1411 /   471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
1441 /   481                1471 /   491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu
```

FIGURE 9D

```
LSN.3'STOP ->   1-phase Translation

DNA sequence   1482 b.p.   CAAGAACAACAA ... ATGAAACTATAA   linear

1 / 1                                                    31 / 11
CAA GAA CAA CAA AGC GAT TTA GAA CAA CAA  CTA GAA CAA CAA GAG AGA CGT GCT AAA GAA
gln glu gln gln ser asp leu glu gln gln  leu glu gln gln glu arg arg ala lys glu

61 / 21                                                  91 / 31
GAA AAG TTG CAA GAA GAA CAA AGC GAT TTA  GAA CAA CAA GAG CAG CAA AGC GAT GAT CAA
glu lys leu gln glu gln gln ser asp leu  glu gln gln glu gln gln ser asp asp gln

121 / 41                                                 151 / 51
AGC GAT TTA GAA CAA CAA GAG AGA CTT GCT  AAA GAA CAA AGC GAT CTA GAA CAA CAA GAG
ser asp leu glu gln gln glu arg leu ala  lys glu gln ser asp leu glu gln gln glu

181 / 61                                                 211 / 71
CAA GAG AGA CTT GCT AAA GAA CAA AGC GAT  TTA GAA CAA CAA GAG CAG CAA AGC GAT CTA
gln glu arg leu ala lys glu gln ser asp  leu glu gln gln glu gln gln ser asp leu

241 / 81                                                 271 / 91
GAG AGA CGT GCT AAA GAA GAA AAG TTG CAA  GAA GAA CAA AGC GAT TTA GAA CAA CAA GAG
glu arg arg ala lys glu glu lys leu gln  glu glu gln ser asp leu glu gln gln glu

301 / 101                                                331 / 111
GCT AAA GAA CTT GCT AAA GAA GAA CAA AGC  GAT TTA GAA CAA GAG CAA CGT GCT AAA GAA
ala lys glu leu ala lys glu glu gln ser  asp leu glu gln glu gln arg ala lys glu

AAG TTG CAA
lys leu gln
```

FIGURE 10A

GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA
glu gln gln ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln gln
121 / 131

391 / 391
AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA
ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu
141 / 151

421 / 451
GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG
glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu
161 / 171

481 / 511
GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG
glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu
181 / 191

541 / 571
AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT
arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu arg arg ala
201 / 211

601 / 631
AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG CAG CAA GAG AGA AAG GCT
lys glu lys leu gln glu gln gln ser asp leu glu gln glu gln gln glu arg lys ala
221 / 231

661 / 691
AAT TTA GAA AGA AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA
asn leu glu arg lys lys glu his gly asp ile leu ala glu asp leu tyr gly arg leu
241 / 251

721 / 751
GAA ATA CCA GCT ATA GAA CTT CCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA
glu ile pro ala ile glu leu pro glu asn glu arg gly tyr tyr ile pro his gln
261 / 271

781 / 811
TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA
ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile

FIGURE 10B

841 / 281
GAA AAA ACA AAT AGA GAA ACA ACA AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA
glu lys thr asn arg glu thr thr asn val glu gly arg arg asp ile his lys
871 / 291
901 / 301
GGA CAT CTT GAA GAA AAG TCT ATT ACA GGT TCA ATA AAA CCA GAA AAA GAA GAT AAA TCT
gly his leu glu glu lys ser ile thr gly ser ile lys pro glu lys glu asp lys ser
931 / 311
961 / 321
GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA
ala asp ile gln asn his thr leu glu thr val asn ile ser asp val asn asp phe gln
991 / 331
1021 / 341
ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA
ile ser lys tyr glu asp glu ile ser ala glu tyr asp asp ser leu ile asp glu glu
1051 / 351
1081 / 361
GAA GAT GAT GAC TTA AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT
glu asp glu asp leu lys pro ile val gln tyr asp asn phe gln asp
1111 / 371
1141 / 381
GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT TTA
glu glu asn ile gly ile tyr lys glu leu glu asp leu ile glu lys asn leu
1171 / 391
1201 / 401
GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA GAA AAA ATA AAA
asp asp leu asp glu gly ile glu lys ser ser glu glu leu ser glu glu lys ile lys
1231 / 411
1261 / 421
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
lys gly lys lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu
1291 / 431

FIGURE 10C

```
1321  /   441               1351  /   451
TAT GAT GAG CAT ATT AAA AAA AAT GAT AAG CAG GTT AAT AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys
1381  /   461               1411  /   471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
1441  /   481               1471  /   491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu
```

FIGURE 10D